

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Corley, Neil C.
Guegler, Karl J.
- (ii) TITLE OF THE INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0333 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 448 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: CORNNOT01
 - (B) CLONE: 45517
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
1      5      10      15
Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp
20      25      30
Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
35      40      45
Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
50      55      60
Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
65      70      75      80
Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
85      90      95
Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
100      105      110
Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
115      120      125
Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
130      135      140
Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
145      150      155      160
Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
165      170      175
Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
180      185      190
Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
195      200      205
Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
210      215      220
Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
225      230      235      240
Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
245      250      255
Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
260      265      270
Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
275      280      285
Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
290      295      300
Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
305      310      315      320
Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
325      330      335
Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
340      345      350
Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
355      360      365
Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
370      375      380
Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
385      390      395      400
Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
405      410      415
Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
420      425      430
Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
435      440      445

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2550 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: CORNNOT01
 (B) CLONE: 45517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCAAGATTGT	TGTGAGGAGT	CTAGCCAGTT	GGTGAGCGCT	GTAATCTGAA	CCAGCTGTGT	60
CCAGACTGAG	GCCCCATTGT	CATTATTTAA	CATACTTAGA	AAATGAAGTG	TTCAATTTTAA	120
ACATTCTCTC	TCCAATTGGT	TTAATGCTGA	ATTACTGAAG	AGGGCTAAGC	AAAACCAGGT	180
GCTTGCCTG	AGGGCTCTGC	AGTGCGTGGG	AGGACCCCGG	CGCTCTCCCC	GTGTCTCTCTC	240
CACGACTCGC	TGCGCCCCCT	TGGAATAAAA	CACCCGCGAG	CCCCGAGGGC	CCAGAGGAGG	300
CCGACGTGCC	CAGGCTCTCT	CGGGGGTCCC	GCCCGCGAGC	TTTCTTCTCG	CCTTCGCATC	360
TCCTCTCTCG	CGCTCTTGGA	CATGCCAGGA	ATAAAAAGGA	TACTCACTGT	TACCATTCTGT	420
GCCTCTCTCT	TTCCAAGCCC	TGGGAATGCA	CAGGCACAGT	GCACGAATGG	CTTTGACCTG	480
GATCGCCAGT	CAGGACAGTG	TTTAGATATT	GATGAATGCC	GAACCATCCC	CGAGGCCCTGC	540
CGAGGAGACA	TGATGTGTGT	TAACCAAAAT	GGCGGGTATT	TATGCATPCC	CCGGACAACAC	600
CCTGTGTATC	GAGGGCCCTA	CTCGAACCCC	TACTCGACCC	CCTACTCAGG	TCCGTATCCCA	660
GCAGCTGTCC	CACCACTCTC	AGCTCCAAAC	TATCCCACGA	TCTCCAGGCC	TCTTATATAG	720
CGCTTTGGAT	ACCAAGATGA	TGAAAGCAAC	CAATGTGTGG	ATGTGGACGA	GTGTGCAACA	780
GATTTCACAC	AGTGCAACCC	CACCCAGATC	TGCATCAATA	CTGAAGCGCG	GTACACCTGC	840
TCCTGCACCG	ACGGATATTG	GCTTCTGGAA	GGCCAGTGCT	TAGACATTGA	TGAATGTCCG	900
TATGGTTACT	GCCACGACCT	CTGTGCGAAT	GTTCCTGGAT	CCTATTCTTG	TACATGCAAC	960
CCTGGTTTFA	CCCTCAATGA	GGATGGAAGG	TCTTGCCAA	ATGTGAACGA	GTGTGCCACC	1020
GAGAACCCCT	CGGTGCAAAC	CTCGCTCAAC	ACCTACGGCT	CTTTCACTGT	CCGCTGTGAC	1080
CCAGGATATG	AACTTGAGGA	AGATGGCGTT	CATTGCAAGT	ATATGGACGA	CTGACTGCTC	1140
TCGTAGTTCC	TCGTCCAACA	TGAGTGTGTG	AACCAGCCCG	GCACATACTT	CTGCTCCTGC	1200
CTCCAGGCT	ACATCTCTCT	GGATGACAAC	CGAAGCTGCC	AAGACATCAA	CGAATGTGAG	1260
CACAGGAACC	ACAGCTGCAA	CTGTCAGCAG	ACGTGCTACA	ATTTACAAGG	GGGCTTCAAA	1320
TGCATCGACC	CCATCCGCTG	TGAGGAGCCCT	TATCTGAGGA	TCAGTGATAA	CCGCTGTATG	1380
TGTCTGTGCT	AGAACCCCTG	CTGCGAGAGC	CAGCCCTTTA	CCATCTTTGA	CCGGGACATG	1440
GAGCTGGTGT	CAGGACGCTC	CGTTCCCGCT	GACATCTTCC	AAATGCAAGC	CACGACCCGC	1500
TACCTTGGGG	CTATTACAT	TTTCCAGATC	AAATCTGGGA	ATGAGGGCAG	AGAAATTTTAC	1560
ATGCGGCAAA	CGGGCCCACT	CAGTGCCACC	CTGGTGATGA	CACGCCCACT	CAAGGGGCCCC	1620
CGGGAAATTC	AGCTGGACTT	GGAAATGATC	ACTGTCAACA	CTGTCAATCAA	CTTCAAGAGC	1680
AGCTCCGTGA	TCCGACTGCG	GATATATGTG	TCGCAGTACC	CATTCTAGAG	CTCGGGCTGG	1740
AGCCTCCGAC	CTGCTCTCTC	ATTGCGACCA	AGGGACAGGA	GAGAGAGAGG	AATAACAGAC	1800
AGAAATGAGG	CGACACAGAC	TTTAGGCATT	TCTTCTGAA	CGTTTCCCCG	AAGAGCTCAG	1860
CCCGACTTCC	TGACTCTCAC	CTGTACTATT	GCAGACCTGT	CACCCCTGAC	GACTTGCCAC	1920
CCCCAGTCT	TATGACACAG	TATCAAAAAA	GTATTATCAT	TGCTCCCTCG	ATAGAAGATT	1980
GTTTGTGAAT	TTTCAAGGCC	TTCACTTTAT	TTCCACTATT	TTCAAAGAAA	ATAGATTAGG	2040
TTTTCGGGGG	TCTGAGCTTA	TGTTCAAAAG	CTGTGAACAG	CTTGTCTGTA	CTTCTTCCAC	2100
CTCTTCAACT	CTTCTCTCAC	TGTTGTACTG	CTTTGCAAA	ACCCGGGAGC	TGGCGGGGAA	2160
CCCTGGGAGT	AGCTAGTTTG	CTTTTTCGCT	ACACAGAGAA	GGCTATGTAA	ACAAACCAAC	2220
CGAGGATCGA	AGGGTTTTTA	GAGAATGTGT	TTCAAAACCA	TGCTTGGTAT	TTTCAACCAT	2280
AAAGAAAGTT	TCAGTTGTTC	TTAAATTTGT	ATAACGGTTT	ATACTCTGCT	TGTTTCATTTT	2340
GAGTATTTTT	AAAAAATATG	TCGTAGAATT	CCTTCTGAA	AGCTTCAGAC	ACATGCTATG	2400
TTCTGTGCTC	CCAAACCCAG	TCTCCTCTCC	ATTTTAGGCC	GCGTCTTTCT	TTGAGGACCC	2460
CTTAATCTTG	CTTCTCTTAG	AATTTTAC	CAATTGGATT	GGAATGCAGA	GGTCTCCAAA	2520
CTGATTAAAT	ATTTGAAGAG	AAAAAATAA				2550

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRAITUT13

(B) CLONE: 1621777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
 1          5          10          15
Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
 20          25          30
Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
 35          40          45
Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
 50          55          60
His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
 65          70          75          80
Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
 85          90          95
Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
100          105          110
Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
115          120          125
Gly Met Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
130          135          140
Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145          150          155          160
Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
165          170          175
Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
180          185          190
Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
195          200          205
Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210          215          220
Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225          230          235          240
Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
245          250          255
Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
260          265          270
Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
275          280          285
Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
290          295          300
Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305          310          315          320
Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
325          330          335
Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
340          345          350
Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
355          360          365
Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His Leu Cys Cys
370          375          380
Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385          390          395          400
Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg
405          410          415
Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
420          425          430

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Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
      435      440      445
Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
      450      455      460
Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465      470      475      480
Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
      485      490      495
Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
500      505      510
Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
515      520      525
Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
530      535      540

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1899 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT13
 (B) CLONE: 162177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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TGGGTGCAAG CTACAACCG TAACAGCCAC CAGACAAGCT TCAGTGGCCG GCCCTTCACA      60
TCCAGACTTG CCTGAGAGGA CCCACCTCTG AGTGTCCAGT GCTCAGTTGC CCCAGGATGG      120
GGACCACAGC CAGAGCAGCC TTGGTCTTGA CCTATTTTGC TGTGTGCTCT GCTGCCTCTG      180
AGGGAGGCTT CACGGCTACA GGACAGAGGC AGCTGAGGCC AGAGCACTTT CAAGAAGPTG      240
GCTACGCAGC TCCCCCTTCC CCACCCCTAT CCGGAAGCCT CCCCATGGAT CACCCTGACT      300
CCTCTCAGCA TGGCCCTCCC TTGAGGGGAC AGAGTCAAGT GCAGCCCCCT CCCTCTCAGG      360
AGGCCACCCC TCTCCAACAG GAAAAGCTGC TACCTGCCCA ACTCCTTGCT GAAAAGGAAG      420
TGGGTCCCCC TCTCCCTCAG GAAGCTGTCC CCCTCCAAAA AGAGCTGCCC TCTCTCCAGC      480
ACCCCAATGA ACAGAAGGAA GGAATGCCAG CTCCATTTCG GGACCAAGGC CATCCAGAAC      540
CTGAGTCCTG GAATGCAGCC CAGCACTGCC AACAGGACCG GTCCCAAGGG GGCTGGGGCC      600
ACCGGCTTGA TGCTTCCCTC CTTGGGCGGC CTCTCCAGA CAACTCTGAAC CAAATCTGCC      660
TTCTTAACCG TACGATGTG GTATATGGTC CCTGGAACCT ACCACAGTCC AGCTACTCCC      720
ACCTCACTCG CAGGGGTGAG ACCCTCAATT TCCTGGAGAT TGGATATTCC CGCTGCTGCC      780
ACTGCCGAGC CCACACAAC CGCCTAGAGT GTGCCAAACT TGTGTGGGAG GAAGCAATGA      840
GCCGATTCTG TGAGGCGGAG TTCTCGGTCA AGACCCGACC CCACTGGTGC TGCACGCGGC      900
AGGGGGAGGC TCGGTTCTCC TGCTTCCAGG AGGAAGCTCC CCAGCCACAC TACCAGCTCC      960
GGGCTTGCCC CAGCCATCAG CCTGATATTT CCTCGGGTCT TGAGCTGCCT TTCCCTCTCTG      1020
GGGTGCCACCT ATTGGACAAT ATCAAGAACA TCTGCCACCT GAGGCGCTTC CGCTCTGTGC      1080
CAGCAACCTC GCCAGCTACT GACCCCTTAC AAAGGGAGCT GCTGGCACTG ATCCAGCTGG      1140
AGAGGGAGTT CAGGCGCTGC TGCCGCCAGG GGAACAATCA CACCTGTACA TGGGAAGGCT      1200
GGGAGGATAC CTTTGACAAA TACTGTGACC GGGAGTATGC TGTGAAGACC CACCACACT      1260
TGTGTGCGCC CACCTCTCCC AGCCCTACTC GGGATGAGTG CTTTGCCCGT CGGCGCTCTT      1320
ACCCCAACTA TGACCGGGAAC ATCTTGACCA TTGACATCGG TCGAGTCACC CCAACCTCA      1380
TGGGCGCACT ATTGGGAAC CAAAGAGTTC TCACCAAGCA TAAACATATT CCTGGGCTGA      1440
TCCACAACAT GACTGCCCGC TGCTGTGACC TGCCATTTC AGAACAGGC TGCTGTGACG      1500
AGGAGGAGAA ATTAACTTTC ATCAATGATC TGTGTGTGCC CCGACGTAAC ATTGTGGCAG      1560
ACCTCGCCTC CTGCTGTTC TCGATCTCTG GGGATGAACA GGTCAACTGC TTCAAGCTCA      1620
ATTATCTGAG GAACGTGCTG CTAGTGCTCT GAGACACTGA GAACGCCAAG GGCCAGGGGG      1680
ACGACGGCTC AACTGGAGGA ACAAAATCA GCTCCACCTC TGAGGCCAAG GAAGAATGAG      1740
TGCACCTAGG GCCTTAGAGG TGCAGATGGG GGAACCCCA CCTTGCCCA CCCATCTGAA      1800
CACTCAATTAC ACTTAACACC TCTTGATTTC GGTGTCTCTA AATGTCTCAC      1860
CCGAGTGTTT TTAAGTGATC CTGTGTGCC TGGCCGAGG      1899

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 458228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Ala Thr Ser Gly Val Leu Pro Gly Gly Phe Val Ala Ser Ala
1      5      10      15
Ala Ala Val Ala Gly Pro Glu Met Gln Thr Gly Arg Asn Phe Val
20     25     30
Ile Arg Arg Asn Pro Ala Asp Pro Gln Arg Ile Pro Ser Asn Pro Ser
35     40     45
His Arg Ile Gln Cys Ala Ala Gly Tyr Glu Gln Ser Glu His Asn Val
50     55     60
Cys Gln Asp Ile Asp Glu Cys Thr Ala Gly Thr His Asn Cys Arg Ala
65     70     75     80
Asp Gln Val Cys Ile Asn Leu Arg Gly Ser Phe Ala Cys Gln Cys Pro
85     90     95
Pro Gly Tyr Gln Lys Arg Gly Glu Gln Cys Val Asp Ile Asp Glu Cys
100    105    110
Thr Ile Pro Pro Tyr Cys His Gln Arg Cys Val Asn Thr Pro Gly Ser
115    120    125
Phe Tyr Cys Gln Cys Ser Pro Gly Phe Gln Leu Ala Ala Asn Asn Tyr
130    135    140
Thr Cys Val Asp Ile Asn Glu Cys Asp Ala Ser Asn Gln Cys Ala Gln
145    150    155    160
Gln Cys Tyr Asn Ile Leu Gly Ser Phe Ile Cys Gln Cys Asn Gln Gly
165    170    175
Tyr Glu Leu Ser Ser Asp Arg Leu Asn Cys Glu Asp Ile Asp Glu Cys
180    185    190
Arg Thr Ser Ser Tyr Leu Cys Gln Tyr Gln Cys Val Asn Glu Pro Gly
195    200    205
Lys Phe Ser Cys Met Cys Pro Gln Gly Tyr Gln Val Val Arg Ser Arg
210    215    220
Thr Cys Gln Asp Ile Asn Glu Cys Glu Thr Thr Asn Glu Cys Arg Glu
225    230    235    240
Asp Glu Met Cys Trp Asn Tyr His Gly Gly Phe Arg Cys Tyr Pro Arg
245    250    255
Asn Pro Cys Gln Asp Pro Tyr Ile Leu Thr Pro Glu Asn Arg Cys Val
260    265    270
Cys Pro Val Ser Asn Ala Met Cys Arg Glu Leu Pro Gln Ser Ile Val
275    280    285
Tyr Lys Tyr Met Ser Ile Arg Ser Asp Arg Ser Val Pro Ser Asp Ile
290    295    300
Phe Gln Ile Gln Ala Thr Thr Ile Tyr Ala Asn Thr Ile Asn Thr Phe
305    310    315    320
Arg Ile Lys Ser Gly Asn Glu Asn Gly Glu Phe Tyr Leu Arg Gln Thr
325    330    335
Ser Pro Val Ser Ala Met Leu Val Leu Val Lys Ser Leu Ser Gly Pro
340    345    350
Arg Glu His Ile Val Asp Leu Glu Met Leu Thr Val Ser Ser Ile Gly
355    360    365

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Thr Phe Arg Thr Ser Ser Val Leu Arg Leu Thr Ile Ile Val Gly Pro
 370 375 380
 Phe Ser Phe
 385

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 496120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Thr Val Ser Arg Ala Ala Leu Ile Leu Ala Cys Leu Ala Leu
 1 5 10 15
 Ala Ser Ala Ala Ser Glu Gly Ala Phe Lys Ala Ser Asp Gln Arg Glu
 20 25 30
 Met Thr Pro Glu Arg Leu Phe Gln His Leu His Glu Val Gly Tyr Ala
 35 40 45
 Ala Pro Pro Ser Leu Pro Gln Thr Arg Arg Leu Arg Val Asp His Ser
 50 55 60
 Val Thr Ser Leu His Asp Pro Pro Leu Phe Glu Gln Arg Glu Val
 65 70 75 80
 Gln Pro Pro Ser Ser Pro Glu Asp Ile Pro Val Tyr Glu Glu Asp Trp
 85 90 95
 Pro Thr Phe Leu Asn Pro Asn Val Asp Lys Ala Gly Pro Ala Val Pro
 100 105 110
 Gln Glu Ala Ile Pro Leu Gln Lys Glu Gln Pro Pro Pro Gln Val His
 115 120 125
 Ile Glu Gln Lys Glu Ile Asp Pro Pro Ala Gln Pro Gln Glu Glu Ile
 130 135 140
 Val Gln Lys Glu Val Lys Pro His Thr Leu Ala Gly Gln Leu Pro Pro
 145 150 155 160
 Glu Pro Arg Thr Trp Asn Pro Ala Arg His Cys Gln Gln Gly Arg Arg
 165 170 175
 Gly Val Trp Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser
 180 185 190
 Pro Asp Asn Leu Lys Gln Ile Cys Leu Pro Glu Arg Gln His Val Ile
 195 200 205
 Tyr Glu Pro Trp Asn Leu Pro Gln Thr Gly Tyr Ser His Leu Ser Arg
 210 215 220
 Gln Gly Glu Thr Leu Asn Val Leu Glu Thr Gly Tyr Ser Arg Cys Cys
 225 230 235 240
 Pro Cys Arg Ser Asp Thr Asn Arg Leu Asp Cys Leu Lys Leu Val Trp
 245 250 255
 Glu Asp Ala Met Thr Gln Phe Cys Glu Ala Glu Phe Ser Val Lys Thr
 260 265 270
 Arg Pro His Leu Cys Cys Arg Leu Arg Gly Glu Glu Arg Phe Ser Cys
 275 280 285
 Phe Gln Lys Glu Ala Pro Arg Pro Asp Tyr Leu Leu Arg Pro Cys Pro
 290 295 300
 Val His Gln Asn Gly Met Ser Ser Gly Pro Gln Leu Pro Phe Pro Pro
 305 310 315 320
 Gly Leu Pro Thr Pro Asp Asn Val Lys Asn Ile Cys Leu Leu Arg Arg
 325 330 335

Phe	Arg	Ala	Val	Pro	Arg	Asn	Leu	Pro	Ala	Thr	Asp	Ala	Ile	Gln	Arg	
		340						345					350			
Gln	Leu	Gln	Ala	Leu	Thr	Arg	Leu	Glu	Thr	Glu	Phe	Gln	Arg	Cys	Cys	
		355						360					365			
Arg	Gln	Gly	His	Asn	His	Thr	Cys	Thr	Trp	Lys	Ala	Trp	Glu	Gly	Thr	
		370						375					380			
Leu	Asp	Gly	Tyr	Cys	Glu	Arg	Glu	Leu	Ala	Ile	Lys	Thr	His	Pro	His	
		385						390					395			400
Ser	Cys	Cys	His	Tyr	Pro	Pro	Ser	Pro	Ala	Arg	Asp	Glu	Cys	Phe	Ala	
				405												415
His	Leu	Ala	Pro	Tyr	Pro	Asn	Tyr	Asp	Arg	Asp	Ile	Leu	Thr	Leu	Asp	
				420												430
Leu	Ser	Arg	Val	Thr	Pro	Asn	Leu	Met	Gly	Gln	Leu	Cys	Gly	Ser	Gly	
				435												445
Arg	Val	Leu	Ser	Lys	His	Lys	Gln	Ile	Pro	Gly	Leu	Ile	Gln	Asn	Met	
				450												460
Thr	Val	Arg	Cys	Cys	Glu	Leu	Pro	Tyr	Pro	Glu	Gln	Ala	Cys	Cys	Gly	
								470								480
Glu	Glu	Glu	Lys	Leu	Ala	Phe	Ile	Glu	Asn	Leu	Cys	Gly	Pro	Arg	Arg	
																495
Asn	Ser	Trp	Lys	Asp	Pro	Ala	Leu	Cys	Cys	Asp	Leu	Ser	Pro	Glu	Asp	
																510
Lys	Gln	Ile	Asn	Cys	Phe	Asn	Thr	Asn	Tyr	Leu	Arg	Asn	Val	Ala	Leu	
																525
Val	Ala	Gly	Asp	Thr	Gly	Asn	Ala	Thr	Gly	Leu	Gly	Glu	Gln	Gly	Pro	
																540
Thr	Arg	Gly	Thr	Asp	Ala	Asn	Pro	Ala	Pro	Gly	Ser	Lys	Glu	Glu		
																555